AMENDMENTS TO THE SPECIFICATION

IN THE SPECIFICATION

On page 37, line 14, please replace the original paragraph with the following amended paragraph:

-- The Gly-Gly-Thr-Gly-Ser-Gly (SEQ ID NO: 82) amino acid sequence in the terminus is part of the linker sequence that was inserted between the NZ zipper peptide and the N-terminal fragments of EGFP (NtermEGFP). The zipper sequence in the NtermEGFP-NZ fusion protein is also Gly-Gly-Thr-Gly-Ser-Gly (SEQ ID NO: 82) with the Gly-Gly-Thr-Gly (residues 1-4 of SEQ ID NO: 82) coding sequence being repeated in the NtermEGFP reverse amplification primers 2129, 2130, and 2131 (Table 3). Underlined are the unique NcoI (CCATGG), AgeI (ACCGGT) and BamHI (GGATCC) sites used for cloning of the zipper peptide into pTrcHis-A and the NtermEGFP-NZ fragments into the NZ zipper vector PS1515 (see below). The asterisk (*) shows a stop codon. --

On page 48, line 8, please replace the original paragraph with the following amended paragraph:

-- Mutagenesis of the eukaryotic NtermEGFP-NZ expression vectors PS1559 (NtermEGFP157-NZ) and PS1560 (NtermEGFP172-NZ) into the corresponding N-terminal EYFP (SEQ ID NO: 5) fragment (NtermEYFP-NZ) variants and mutagenesis of the eukaryotic CtermEGFP expression vectors PS1557 (CZ-CtermEGFP158) and PS1558 (CZ-CtermEGFP173) into the corresponding C-terminal EYFP fragment (CZ-CtermEYFP) variants was accomplished by site directed mutagenesis using the QuickChange kit and by following the manufacturers instructions (Stratagene). Primers 2333 and 2334 were used to convert expression vectors PS1559 (NtermEGFP157-NZ) and PS1560 (NtermEGFP172-

NZ) into N-terminal EYFP fragment expression vectors PS1639 (NtermEYFP157-NZ) and PS1642 (NtermEYFP172-NZ). The introduced mutations were: L64F:T65G:V68L:S72A. Furthermore, primers 2335 and 2336 were used to convert expression vectors PS1559 (NtermEGFP157-NZ) and PS1560 (NtermEGFP172-NZ) into F64L mutated N-terminal EYFP fragment expression vectors PS1640 (NtermE[F64L]YFP157-NZ) and PS1641 (NtermE[F64L]YFP172-NZ). The introduced mutations were: T65G:V68L:S72A. Accordingly, the expressed NtermEYFP fragments have the following amino acid sequences (SEQ ID NOS: 78-80)(only residues 64-72 are shown): --

On page 51, line 19, please replace the original paragraph with the following amended paragraph:

-- PS1641 was subjected to PCR with primers 2219 and 2222 (Table 2), and the ca 0.5 kb Nhe1-BamH1 fragment was ligated into pEGFP-C1 (Clontech) digested with Nhe1 and BamH1. This replaces NtermEGFP with NtermE[F64L]YFP172 followed by a linker sequence, which encodes in frame linker sequence Gly-Ser-Gly-Ser-Gly-Ser-Gly (SEQ ID NO: 81), and a unique EcoRV site just upstream of BamH1. This plasmid is called PS1672. --

On page 53, line 5, please replace the original paragraph with the following amended paragraph:

-- PS1638 was subjected to PCR with primers 2225 and 2132 (Table 2), and the ca 0.25 kb Nhe1-BamH1 fragment was ligated into PS609 digested with Nhe1 and BamH1. This replaces EGFP with EYFP(173-238) preceded by a linker sequence, which encodes in frame linker sequence Gly-Ser-Gly-Ser-Gly-Ser-Gly (SEQ ID NO: 81), and a unique EcoRV site just downstream of Nhe1. This plasmid is called PS1674.--

On page 59, line 13, please replace the original paragraph with the following amended paragraph:

-- PS1641 was subjected to PCR with primers 2219 and 2387 (table 2), and the ca 0.5 kb Nhe1-BamH1 fragment was ligated into pEGFP-C1 (Clontech) digested with Nhe1 and BamH1. This replaces EGFP with F64L,EYFP(1-172)followed by a linker sequence, which encodes in frame linker sequence GGTGSG(SEQ ID NO: 82)-NZ-GSGSGSG(SEQ ID NO: 81), and a unique EcoRV site just upstream of BamH1. This plasmid is called PS1673. --

On page 60, line 9, please replace the original paragraph with the following amended paragraph:

--PS1638 was subjected to PCR with primers 2388 and 2132 (table 2), and the ca 0.35 kb Nhe1-BamH1 fragment was ligated into PS609 digested with Nhe1 and BamH1. This replaces EGFP with EYFP(173-238)preceded by a linker sequence, which encodes in frame linker sequence GSGSGSG(SEQ ID NO: 81)-zip, and a unique EcoRV site just downstream of Nhe1. This plasmid is called PS1726. --

On page 61, line 23, please replace the original paragraph with the following amended paragraph:

-- The coding sequence of H2B (GenBank Acc no NM_003518) was isolated from human cDNA with primers 2389 and 2390 (Table 2), and the ca 0.4 kb Nhe1-EcoRV fragment was ligated into PS1674 digested with Nhe1 and EcoRV. This places H2B upstream of EYFP(173-238), which is preceded by a linker sequence, which encodes in frame linker sequence GSGSGSG(SEQ ID NO: 81)-

zip, and a unique EcoRV site between H2B and the linker-EYFP(173-238). This plasmid is called PS1790. --

On page 62, line 24, please replace the original paragraph with the following amended paragraph:

-- PS1768 was subjected to PCR with primers 2462 and 2463, and the ca 0.35 kb fragment was digested with Pvu2 and BamH1 and ligated into PS1672 digested with EcoRV and BamH1. This produces a fusion of F64L,NY172 and FKBP connected by a GSGSGSGDL(SEQ ID NO: 72) linker and with a GTGTGTG(SEQ ID NO: 83) linker sequence behind FKBP and a unique EcoRV site just downstream of the GT3 linker. This plasmid is called PS1789. --

On page 63, line 17, please replace the original paragraph with the following amended paragraph:

-- PS1767 was subjected to PCR with primers 2464 and 2465, and the ca 0.35 kb product was digested with Nhe1-Sma1 and ligated into PS1674 digested with Nhe1 and EcoRV. This produces a fusion of FRAP(2025-2114) and EYFP(173-238) connected by a linker sequence, GSGSGSG(SEQ ID NO: 81), and with a GTGTGTG(SEQ ID NO: 83) linker sequence in front of FRAP, and a unique EcoRV site just upstream of the GTGTGTG(SEQ ID NO: 83) linker. This plasmid is called PS1788. --

On page 79, line 20, please replace the original paragraph with the following amended paragraph:

-- Alignment of fluorescent proteins (SEQ ID NOS: 84-99). --